

10/546000

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SEQUENCE LISTING

<110> DNAVAC RESEARCH INC.

<120> Method of treating ischemic disease

<130> D3-A0208P

<150> JP 2003-040806

<151> 2003-02-19

<160> 9

<170> PatentIn version 3.1

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<213> Homo sapiens

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Ser Gly Thr Val Glu Gly Ala Met Asp Leu Ile Leu Ile Asn Ser Leu
20 25 30

cct ctt gta tct gat gct gaa aca tct ctc acc tgc att gcc tct ggg 144
Pro Leu Val Ser Asp Ala Glu Thr Ser Leu Thr Cys Ile Ala Ser Gly
35 40 45

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Trp Arg Pro His Glu Pro Ile Thr Ile Gly Arg Asp Phe Glu Ala Leu

50	55	60	
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85	90		95
aat ggt gct tat ttc tgt gaa ggg cga gtt cga gga gag gca atc agg Asn Gly Ala Tyr Phe Cys Glu Gly Arg Val Arg Gly Glu Ala Ile Arg			336
100	105	110	
ata cga acc atg aag atg cgt caa caa gct tcc ttc cta cca gct act Ile Arg Thr Met Lys Met Arg Gln Gln Ala Ser Phe Leu Pro Ala Thr			384
115	120	125	
tta act atg act gtg gac aag gga gat aac gtg aac ata tct ttc aaa Leu Thr Met Thr Val Asp Lys Gly Asp Asn Val Asn Ile Ser Phe Lys			432
130	135	140	
aag gta ttg att aaa gaa gaa gat gca gtg att tac aaa aat ggt tcc Lys Val Leu Ile Lys Glu Glu Asp Ala Val Ile Tyr Lys Asn Gly Ser			480
145	150	155	160
ttc atc cat tca gtg ccc cgg cat gaa gta cct gat att cta gaa gta Phe Ile His Ser Val Pro Arg His Glu Val Pro Asp Ile Leu Glu Val			528
165	170	175	
cac ctg cct cat gct cag ccc cag gat gct gga gtg tac tcg gcc agg His Leu Pro His Ala Gln Pro Gln Asp Ala Gly Val Tyr Ser Ala Arg			576
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225	230	235	240
att tgc cct cct ggg ttt atg gga agg acg tgt gag aag gct tgt gaa Ile Cys Pro Pro Gly Phe Met Gly Arg Thr Cys Glu Lys Ala Cys Glu			768
245	250	255	
ctg cac acg ttt ggc aga act tgt aaa gaa agg tgc agt gga caa gag Leu His Thr Phe Gly Arg Thr Cys Lys Glu Arg Cys Ser Gly Gln Glu			816
260	265	270	
gga tgc aag tct tat gtg ttc tgt ctc cct gac ccc tat ggg tgt tcc Gly Cys Lys Ser Tyr Val Phe Cys Leu Pro Asp Pro Tyr Gly Cys Ser			864
275	280	285	
tgt gcc aca ggc tgg aag ggt ctg cag tgc aat gaa gca tgc cac cct Cys Ala Thr Gly Trp Lys Gly Leu Gln Cys Asn Glu Ala Cys His Pro			912
290	295	300	
ggt ttt tac ggg cca gat tgt aag ctt agg tgc agc tgc aac aat ggg Gly Phe Tyr Gly Pro Asp Cys Lys Leu Arg Cys Ser Cys Asn Asn Gly			960
305	310	315	320
gag atg tgt gat cgc ttc caa gga tgt ctc tgc tct cca gga tgg cag Glu Met Cys Asp Arg Phe Gln Gly Cys Leu Cys Ser Pro Gly Trp Gln			1008
325	330	335	
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Leu Thr Trp Gln Pro Ile Phe Pro Ser Ser Glu Asp Asp Phe Tyr Val			
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Val Pro Gly Asn Leu Thr Ser Val Leu Leu Asn Asn Leu His Pro Arg			
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caa cca gaa aac atc aag att tcc aac att aca cac tcc tcg gct gtg			1968
Gln Pro Glu Asn Ile Lys Ile Ser Asn Ile Thr His Ser Ser Ala Val			
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Ile Ser Trp Thr Ile Leu Asp Gly Tyr Ser Ile Ser Ser Ile Thr Ile			
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Arg Tyr Lys Val Gln Gly Lys Asn Glu Asp Gln His Val Asp Val Lys			
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Ile Lys Asn Ala Thr Ile Ile Gln Tyr Gln Leu Lys Gly Leu Glu Pro			

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835	840	845	
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gcc aat agc acc gcg tcc aca ctg tcc tcc cag cag ctc ctt cac ttc 2832 Ala Asn Ser Thr Ala Ser Thr Leu Ser Ser Gln Gln Leu Leu His Phe 930 935 940			
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gtg gca aaa ata gca gat ttt gga ttg tcc cga ggt caa gag gtg tac 2976 Val Ala Lys Ile Ala Asp Phe Gly Leu Ser Arg Gly Gln Glu Val Tyr 980 985 990			
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1040	1045	1050	
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1070	1075	1080	
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1085	1090	1095	
cga aag acc tac gtg aat acc acg ctt tat gag aag ttt act tat Arg Lys Thr Tyr Val Asn Thr Thr Leu Tyr Glu Lys Phe Thr Tyr			3339
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Met Asn Gln His Gln Asp Pro Leu Glu Val Thr Gln Asp Val Thr Arg
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Glu Trp Ala Lys Lys Val Val Trp Lys Arg Glu Lys Ala Ser Lys Ile
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Ile Arg Thr Met Lys Met Arg Gln Gln Ala Ser Phe Leu Pro Ala Thr
 115 120 125

Leu Thr Met Thr Val Asp Lys Gly Asp Asn Val Asn Ile Ser Phe Lys
 130 135 140

Lys Val Leu Ile Lys Glu Glu Asp Ala Val Ile Tyr Lys Asn Gly Ser
 145 150 155 160

Phe Ile His Ser Val Pro Arg His Glu Val Pro Asp Ile Leu Glu Val
 165 170 175

His Leu Pro His Ala Gln Pro Gln Asp Ala Gly Val Tyr Ser Ala Arg
 180 185 190

Tyr Ile Gly Gly Asn Leu Phe Thr Ser Ala Phe Thr Arg Leu Ile Val
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Arg Arg Cys Glu Ala Gln Lys Trp Gly Pro Glu Cys Asn His Leu Cys
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275	280		285
Cys Ala Thr Gly Trp Lys Gly Leu Gln Cys Asn Glu Ala Cys His Pro			
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Gly Phe Tyr Gly Pro Asp Cys Lys Leu Arg Cys Ser Cys Asn Asn Gly			
305	310	315	320
Glu Met Cys Asp Arg Phe Gln Gly Cys Leu Cys Ser Pro Gly Trp Gln			
325	330		335
Gly Leu Gln Cys Glu Arg Glu Gly Ile Pro Arg Met Thr Pro Lys Ile			
340	345		350
Val Asp Leu Pro Asp His Ile Glu Val Asn Ser Gly Lys Phe Asn Pro			
355	360		365
Ile Cys Lys Ala Ser Gly Trp Pro Leu Pro Thr Asn Glu Glu Met Thr			
370	375		380
Leu Val Lys Pro Asp Gly Thr Val Leu His Pro Lys Asp Phe Asn His			
385	390	395	400
Thr Asp His Phe Ser Val Ala Ile Phe Thr Ile His Arg Ile Leu Pro			
405	410		415
Pro Asp Ser Gly Val Trp Val Cys Ser Val Asn Thr Val Ala Gly Met			
420	425		430
Val Glu Lys Pro Phe Asn Ile Ser Val Lys Val Leu Pro Lys Pro Leu			
435	440		445

Asn Ala Pro Asn Val Ile Asp Thr Gly His Asn Phe Ala Val Ile Asn
450 455 460

Ile Ser Ser Glu Pro Tyr Phe Gly Asp Gly Pro Ile Lys Ser Lys Lys
465 470 475 480

Leu Leu Tyr Lys Pro Val Asn His Tyr Glu Ala Trp Gln His Ile Gln
485 490 495

Val Thr Asn Glu Ile Val Thr Leu Asn Tyr Leu Glu Pro Arg Thr Glu
500 505 510

Tyr Glu Leu Cys Val Gln Leu Val Arg Arg Gly Glu Gly Gly Glu Gly
515 520 525

His Pro Gly Pro Val Arg Arg Phe Thr Thr Ala Ser Ile Gly Leu Pro
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Leu Thr Trp Gln Pro Ile Phe Pro Ser Ser Glu Asp Asp Phe Tyr Val
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580 585 590

Val Pro Gly Asn Leu Thr Ser Val Leu Leu Asn Asn Leu His Pro Arg
595 600 605

Glu Gln Tyr Val Val Arg Ala Arg Val Asn Thr Lys Ala Gln Gly Glu
610 615 620

Trp Ser Glu Asp Leu Thr Ala Trp Thr Leu Ser Asp Ile Leu Pro Pro
625 630 635 640

Gln Pro Glu Asn Ile Lys Ile Ser Asn Ile Thr His Ser Ser Ala Val
645 650 655

Ile Ser Trp Thr Ile Leu Asp Gly Tyr Ser Ile Ser Ser Ile Thr Ile
 660 665 670

Arg Tyr Lys Val Gln Gly Lys Asn Glu Asp Gln His Val Asp Val Lys
 675 680 685

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 690 695 700

Glu Thr Ala Tyr Gln Val Asp Ile Phe Ala Glu Asn Asn Ile Gly Ser
 705 710 715 720

Ser Asn Pro Ala Phe Ser His Glu Leu Val Thr Leu Pro Glu Ser Gln
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Ala Pro Ala Asp Leu Gly Gly Lys Met Leu Leu Ile Ala Ile Leu
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Gly Ser Ala Gly Met Thr Cys Leu Thr Val Leu Leu Ala Phe Leu Ile
 755 760 765

Ile Leu Gln Leu Lys Arg Ala Asn Val Gln Arg Arg Met Ala Gln Ala
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Phe Gln Asn Val Arg Glu Glu Pro Ala Val Gln Phe Asn Ser Gly Thr
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Leu Ala Leu Asn Arg Lys Val Lys Asn Asn Pro Asp Pro Thr Ile Tyr
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Pro Val Leu Asp Trp Asn Asp Ile Lys Phe Gln Asp Val Ile Gly Glu
 820 825 830

Gly Asn Phe Gly Gln Val Leu Lys Ala Arg Ile Lys Lys Asp Gly Leu
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Arg Met Asp Ala Ala Ile Lys Arg Met Lys Glu Tyr Ala Ser Lys Asp
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Asp His Arg Asp Phe Ala Gly Glu Leu Glu Val Leu Cys Lys Leu Gly

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Tyr Leu Tyr Leu Ala Ile Glu Tyr Ala Pro His Gly Asn Leu Leu Asp			
900	905		910
Phe Leu Arg Lys Ser Arg Val Leu Glu Thr Asp Pro Ala Phe Ala Ile			
915	920		925
Ala Asn Ser Thr Ala Ser Thr Leu Ser Ser Gln Gln Leu Leu His Phe			
930	935		940
Ala Ala Asp Val Ala Arg Gly Met Asp Tyr Leu Ser Gln Lys Gln Phe			
945	950	955	960
Ile His Arg Asp Leu Ala Ala Arg Asn Ile Leu Val Gly Glu Asn Tyr			
965	970		975
Val Ala Lys Ile Ala Asp Phe Gly Leu Ser Arg Gly Gln Glu Val Tyr			
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Val Lys Lys Thr Met Gly Arg Leu Pro Val Arg Trp Met Ala Ile Glu			
995	1000		1005
Ser Leu Asn Tyr Ser Val Tyr Thr Thr Asn Ser Asp Val Trp Ser			
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Tyr Gly Val Leu Leu Trp Glu Ile Val Ser Leu Gly Gly Thr Pro			
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Tyr Cys Gly Met Thr Cys Ala Glu Leu Tyr Glu Lys Leu Pro Gln			
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Asp Leu Met Arg Gln Cys Trp Arg Glu Lys Pro Tyr Glu Arg Pro			
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Ser Phe Ala Gln Ile Leu Val Ser Leu Asn Arg Met Leu Glu Glu
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 Ile Gly Cys Ser Asn Gln Arg Arg Ser Pro Glu Asn Ser Gly Arg Arg
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tat aac cgg att caa cat ggg caa tgt gcc tac act ttc att ctt cca 144
 Tyr Asn Arg Ile Gln His Gly Gln Cys Ala Tyr Thr Phe Ile Leu Pro
 35 40 45

gaa cac gat ggc aac tgt cgt gag agt acg aca gac cag tac aac aca 192
 Glu His Asp Gly Asn Cys Arg Glu Ser Thr Thr Asp Gln Tyr Asn Thr
 50 55 60

aac gct ctg cag aga gat gct cca cac gtg gaa ccg gat ttc tct tcc 240
 Asn Ala Leu Gln Arg Asp Ala Pro His Val Glu Pro Asp Phe Ser Ser

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cag aaa ctt caa cat ctg gaa cat gtg atg gaa aat tat act cag tgg Gln Lys Leu Gln His Leu Glu His Val Met Glu Asn Tyr Thr Gln Trp				288
85	90	95		
ctg caa aaa ctt gag aat tac att gtg gaa aac atg aag tcg gag atg Leu Gln Lys Leu Glu Asn Tyr Ile Val Glu Asn Met Lys Ser Glu Met				336
100	105	110		
gcc cag ata cag cag aat gca gtt cag aac cac acg gct acc atg ctg Ala Gln Ile Gln Gln Asn Ala Val Gln Asn His Thr Ala Thr Met Leu				384
115	120	125		
gag ata gga acc agc ctc ctc tct cag act gca gag cag acc aga aag Glu Ile Gly Thr Ser Leu Leu Ser Gln Thr Ala Glu Gln Thr Arg Lys				432
130	135	140		
ctg aca gat gtt gag acc cag gta cta aat caa act tct cga ctt gag Leu Thr Asp Val Glu Thr Gln Val Leu Asn Gln Thr Ser Arg Leu Glu				480
145	150	155	160	
ata cag ctg ctg gag aat tca tta tcc acc tac aag cta gag aag caa Ile Gln Leu Leu Glu Asn Ser Leu Ser Thr Tyr Lys Leu Glu Lys Gln				528
165	170	175		
ctt ctt caa cag aca aat gaa atc ttg aag atc cat gaa aaa aac agt Leu Leu Gln Gln Thr Asn Glu Ile Leu Lys Ile His Glu Lys Asn Ser				576
180	185	190		
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195	200	205		
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210	215	220		
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245		250		255
aca gtc cac aac ctt gtc aat ctt tgc act aaa gaa ggt gtt tta cta Thr Val His Asn Leu Val Asn Leu Cys Thr Lys Glu Gly Val Leu Leu				816
260		265		270
aag gga gga aaa aga gag gaa gag aaa cca ttt aga gac tgt gca gat Lys Gly Gly Lys Arg Glu Glu Lys Pro Phe Arg Asp Cys Ala Asp				864
275		280		285
gta tat caa gct ggt ttt aat aaa agt gga atc tac act att tat att Val Tyr Gln Ala Gly Phe Asn Lys Ser Gly Ile Tyr Thr Ile Tyr Ile				912
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305		310		315
320				
ggg gga ggt tgg act gta ata caa cat cgt gaa gat gga agt cta gat Gly Gly Gly Trp Thr Val Ile Gln His Arg Glu Asp Gly Ser Leu Asp				1008
325		330		335
ttc caa aga ggc tgg aag gaa tat aaa atg ggt ttt gga aat ccc tcc Phe Gln Arg Gly Trp Lys Glu Tyr Lys Met Gly Phe Gly Asn Pro Ser				1056
340		345		350
ggt gaa tat tgg ctg ggg aat gag ttt att ttt gcc att acc agt cag Gly Glu Tyr Trp Leu Gly Asn Glu Phe Ile Phe Ala Ile Thr Ser Gln				1104
355		360		365
agg cag tac atg cta aga att gag tta atg gac tgg gaa ggg aac cga Arg Gln Tyr Met Leu Arg Ile Glu Leu Met Asp Trp Glu Gly Asn Arg				1152
370		375		380
gcc tat tca cag tat gac aga ttc cac ata gga aat gaa aag caa aac Ala Tyr Ser Gln Tyr Asp Arg Phe His Ile Gly Asn Glu Lys Gln Asn				1200

385	390	395	400	
tat agg ttg tat tta aaa ggt cac act ggg aca gca gga aaa cag agc				1248
Tyr Arg Leu Tyr Leu Lys Gly His Thr Gly Thr Ala Gly Lys Gln Ser				
405		410		415
agc ctg atc tta cac ggt gct gat ttc agc act aaa gat gct gat aat				1296
Ser Leu Ile Leu His Gly Ala Asp Phe Ser Thr Lys Asp Ala Asp Asn				
420		425		430
gac aac tgt atg tgc aaa tgt gcc ctc atg tta aca gga gga tgg tgg				1344
Asp Asn Cys Met Cys Lys Cys Ala Leu Met Leu Thr Gly Gly Trp Trp				
435		440		445
ttt gat gct tgt ggc ccc tcc aat cta aat gga atg ttc tat act gcg				1392
Phe Asp Ala Cys Gly Pro Ser Asn Leu Asn Gly Met Phe Tyr Thr Ala				
450		455		460
gga caa aac cat gga aaa ctg aat ggg ata aag tgg cac tac ttc aaa				1440
Gly Gln Asn His Gly Lys Leu Asn Gly Ile Lys Trp His Tyr Phe Lys				
465		470		475
480				
ggg ccc agt tac tcc tta cgt tcc aca act atg atg att cga cct tta				1488
Gly Pro Ser Tyr Ser Leu Arg Ser Thr Thr Met Met Ile Arg Pro Leu				
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gat ttt				1494
Asp Phe				

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 <211> 498
 <212> PRT
 <213> Homo sapiens

<400> 4
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Tyr	Asn	Arg	Ile	Gln	His	Gly	Gln	Cys	Ala	Tyr	Thr	Phe	Ile	Leu	Pro
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Glu	His	Asp	Gly	Asn	Cys	Arg	Glu	Ser	Thr	Thr	Asp	Gln	Tyr	Asn	Thr
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Asn	Ala	Leu	Gln	Arg	Asp	Ala	Pro	His	Val	Glu	Pro	Asp	Phe	Ser	Ser
65															80
Gln	Lys	Leu	Gln	His	Leu	Glu	His	Val	Met	Glu	Asn	Tyr	Thr	Gln	Trp
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Glu	Ile	Gly	Thr	Ser	Leu	Leu	Ser	Gln	Thr	Ala	Glu	Gln	Thr	Arg	Lys
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Leu	Leu	Gln	Gln	Thr	Asn	Glu	Ile	Leu	Lys	Ile	His	Glu	Lys	Asn	Ser
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Leu	Asp	Thr	Leu	Lys	Glu	Glu	Lys	Glu	Asn	Leu	Gln	Gly	Leu	Val	Thr
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Arg	Gln	Thr	Tyr	Ile	Ile	Gln	Glu	Leu	Glu	Lys	Gln	Leu	Asn	Arg	Ala

225	230	235	240
Thr Thr Asn Asn Ser Val Leu Gln Lys Gln Gln Leu Glu Leu Met Asp			
245		250	255
Thr Val His Asn Leu Val Asn Leu Cys Thr Lys Glu Gly Val Leu Leu			
260	265	270	
Lys Gly Gly Lys Arg Glu Glu Lys Pro Phe Arg Asp Cys Ala Asp			
275	280	285	
Val Tyr Gln Ala Gly Phe Asn Lys Ser Gly Ile Tyr Thr Ile Tyr Ile			
290	295	300	
Asn Asn Met Pro Glu Pro Lys Lys Val Phe Cys Asn Met Asp Val Asn			
305	310	315	320
Gly Gly Gly Trp Thr Val Ile Gln His Arg Glu Asp Gly Ser Leu Asp			
325	330	335	
Phe Gln Arg Gly Trp Lys Glu Tyr Lys Met Gly Phe Gly Asn Pro Ser			
340	345	350	
Gly Glu Tyr Trp Leu Gly Asn Glu Phe Ile Phe Ala Ile Thr Ser Gln			
355	360	365	
Arg Gln Tyr Met Leu Arg Ile Glu Leu Met Asp Trp Glu Gly Asn Arg			
370	375	380	
Ala Tyr Ser Gln Tyr Asp Arg Phe His Ile Gly Asn Glu Lys Gln Asn			
385	390	395	400
Tyr Arg Leu Tyr Leu Lys Gly His Thr Gly Thr Ala Gly Lys Gln Ser			
405	410	415	
Ser Leu Ile Leu His Gly Ala Asp Phe Ser Thr Lys Asp Ala Asp Asn			
420	425	430	
Asp Asn Cys Met Cys Lys Cys Ala Leu Met Leu Thr Gly Gly Trp Trp			
435	440	445	

Phe Asp Ala Cys Gly Pro Ser Asn Leu Asn Gly Met Phe Tyr Thr Ala
 450 455 460

Gly Gln Asn His Gly Lys Leu Asn Gly Ile Lys Trp His Tyr Phe Lys
 465 470 475 480

Gly Pro Ser Tyr Ser Leu Arg Ser Thr Thr Met Met Ile Arg Pro Leu
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<212> DNA

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<220>

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catg	1744

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<220>
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<400> 6
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<211> 24
<212> DNA
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<220>
<223> an artificially synthesized primer

<400> 7
agatgctcaa ggggcttcat gatg 24

<210> 8

<211> 20
<212> DNA
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<220>
<223> an artificially synthesized primer

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20

<210> 9
<211> 20
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<213> Artificial

<220>
<223> an artificially synthesized primer

<400> 9
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20